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General Physiology is the study of biological mechanisms through analytical investigations, which decipher the molecular and cellular mechanisms underlying biological function at all levels of organization.

The mission of the *Journal of General Physiology* is to publish articles that elucidate important biological, chemical, or physical mechanisms of broad physiological significance.

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Cover picture: Partial separation of degenerate site in asymmetrical ABC exporter. Ribbon diagram of nucleotide-binding domain dimer from crystal structure of TM287/288 (green/blue; Protein Data Bank accession no. 3QF4) with AMPPNP (yellow) bound at the degenerate site. Corresponding Walker A threonines (red) and D-loop residues TM288/N521 and TM287/S499 (violet) are in space fill. The empty active site is wide open, and the nucleotide-bound degenerate site retains some inter-NBD contact through opposing Walker A and D-loops. This figure was generated with PyMOL Molecular Graphics System (see research article by Csanády et al., 61–73).

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Cover picture: Electrophysiologically benign antibodies can be chemically modified for targeted inhibition of ionic currents. On the cover, the exquisite specificity of one such anti-channel monoclonal antibody can be seen by immunohistochemical analysis in brain. Double-label immunofluorescence staining for anti-Kv4.2 monoclonal antibody (red) and anti-Kv2.1 polyclonal antibody (green) in sections prepared from the brains of wild-type (top row) and Kv4.2 knockout (bottom row) mice (see Communication by Sack et al., 315–324).

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Cover picture: FRET spectroscopy measurement of protein interactions in hERG K^+ channels. Wide-field (left, top and bottom) and spectroscopic (middle, top and bottom) images of HEK293 cells coexpressing hERG N-terminal eag domains fused to CFP and hERG channels (with a deletion of the eag domain) fused to Citrine. (Right) Plot of spectroscopic data and spectral separation analysis indicating robust FRET between the two proteins (see research article by Gianulis et al., 351–366).

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Cover picture: (Left) Scanning electron micrographs of an outer hair cell hair bundle from a mouse harboring null mutations in transmembrane channel–like protein isoforms 1 and 2. The bundle possesses tip links (bottom, arrows) thought to deliver force to the mechanotransducer channels. (Right) Mechanotransducer currents in mutants, unlike those in wild type, are activated by negative deflections of the bundle and are insensitive to BAPTA (see research article by Kim et al., 493–505).

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Cover picture: Crystal structure of E118A KcsA mutant shows that the absence of the glutamate leads to changes in the position and order of two nearby arginines, supporting conclusions from functional data that these three residues interact during gating. The figure shows an alignment of the second transmembrane domain C termini between WT and the E118A mutant structures, with the relevant residues highlighted (see research article by Posson et al., 613–624).